

## Sequence Comparison C

RESULT 1  
JN0621  
G protein-coupled receptor type B - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 19-May-2000  
C;Accession: JN0621  
R;Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.  
Biochem. Biophys. Res. Commun. 194, 504-511, 1993  
A;Title: Identification of novel members of G-protein coupled receptor superfamily  
expressed in bovine taste tissue.  
A;Reference number: JN0621; MUID:93326166  
A;Accession: JN0621  
A;Molecule type: mRNA  
A;Residues: 1-350 <MAT>  
A;Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711  
A;Experimental source: tongue taste papillae  
C;Comment: This protein is involved in modulating taste sensitivity or regeneration of  
taste cells.  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein  
F;42-66/Domain: transmembrane #status predicted <TM1>  
F;80-99/Domain: transmembrane #status predicted <TM2>  
F;114-135/Domain: transmembrane #status predicted <TM3>  
F;154-175/Domain: transmembrane #status predicted <TM4>  
F;200-222/Domain: transmembrane #status predicted <TM5>  
F;242-265/Domain: transmembrane #status predicted <TM6>  
F;284-306/Domain: transmembrane #status predicted <TM7>  
F;6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1%; Score 1620; DB 2; Length 350;  
Best Local Similarity 86.0%; Pred. No. 1.1e-131;  
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

Qy	1 MALEQNQSTDYYYYEENEMNGTYDYSQYBLICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
	:              : :   :   :   :   :   :   :   :   :   :   :
Db	1 MAVEYNQSTDYYYYEENEMNDTHDYSQYEVICIKEEVRKFAKVFLPAFFTIAFIIGLAGNS 60
Qy	61 MVVAIYAYYKKQRTKTDVYILNLAVADLLLFTLPFWAVNAVHGWLKGKIMCKITSALYT 120
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	61 TVVVAIYAYYKKRRTKTDVYILNLAVADLFLLFTLPFWAVNAVHGWLKGKIMCKVTSALYT 120
Qy	121 LNFVSGMQFLACISIDRYVAVTKVPSQSGVGKPCWIICFCVWMAAILLSIPQLVFYTVND 180
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	121 VNFVSGMQFLACISTDRYWAVTKAPSQSGVGKPCWVICFCVWAAILLSIPQLVFYTVNH 180
Qy	181 NARCIPIFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFITARTLMKMPNIKISRPLK 240
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	181 KARCVPIFPYHGTSMKASIQILEICIGFIIPFLIMAVCYFITAKTLIKMPNIKKSQPLK 240
Qy	241 VLLTVVIVFIVTQLPYNIVKFCRAIDIYSLITSCNMSKRMEDIAIQVTEISIALFHSCLNP 300
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	241 VLFTVVIVFIVTQLPYNIVKFCQADIIYSLITDCDMSKRMEDIAIQITESIALFHSCLNP 300
Qy	301 ILYVFMGASFKNYVMKVAKKYGSWRRQRQSVEEFPFDSEGPTEPTSTFSI 350
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	301 VLYVFMGTSFKNYIMKVAKKYGSWRRQRQNVEEIPFESEDATEPTSTFSI 350